RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/532.197
Source:	P.C.
Date Processed by STIC:	2/9/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial	Number: 10/532,197	CRF Edit Date: 2/9/06 Edited by:
	Realigned nucleic acid/amino acid numbers/text text "wrapped" to the next line	in cases where the sequence
	Corrected the SEQ ID NO. Sequence numbers e	edited were:
	Inserted or corrected a nucleic number at the en NO's edited:	d of a nucleic line. SEQ ID
	Deleted: invalid beginning/end-of-file text;	page numbers
	Inserted mandatory headings/numeric identifier	s, specifically:
	Moved responses to same line as heading/numeri	ic identifier, specifically:
_	Other: Seguese It-corrected amend	acid rumbering

Revised 09/09/2003



PCT

RAW SEQUENCE LISTING DATE: 02/09/2006
PATENT APPLICATION: US/10/532,197 TIME: 18:29:57

Input Set : A:\PTO.AMC.txt

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              Prentice, Holly
       <120> TITLE OF INVENTION: HIGH EXPRESSION LOCUS VECTOR BASED ON
              FERRITIN HEAVY CHAIN GENE LOCUS
     11 <130> FILE REFERENCE: 2159.058PC01/EKS/LMB
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/532,197
C--> 13 <141> CURRENT FILING DATE: 2005-04-21
     13 <150> PRIOR APPLICATION NUMBER: PCT/US2003/033433
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     16 <150> PRIOR APPLICATION NUMBER: US 60/421,252
     17 <151> PRIOR FILING DATE: 2002-10-24
     19 <160> NUMBER OF SEQ ID NOS: 41
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     36 acgttetege ceagagtege egeggtttee tgetteaaca gtgettgaac ggaacceggt
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     37 getegacece teegaceeee gteeggeege tttgageetg agecetttge aacttegteg
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     38 ctccgccgct ccagcgtcgc ctccgcgcct cgtccagccg ccatc atg acc acc gcg
    39
                                                           Met Thr Thr Ala
     40
     42 tot coo tog caa gtg cgc cag aac tac cac cag gac tog gag got goo
                                                                               405
     43 Ser Pro Ser Gln Val Arg Gln Asn Tyr His Gln Asp Ser Glu Ala Ala
                                                                      20
     44
       5
                             10
                                                                               453
     46 atc aac cgc cag atc aac ctg gag ttg tat gcc tcc tac gtc tat ctg
     47 Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser Tyr Val Tyr Leu
                                             30
                                                                  35
     48
                         25
                                                                              509
     50 tcc atg gtgagtgcgg cctggccttt gcgggggcgg aaagagggtg cggcctggcc
     51 Ser Met
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Input Set : A:\PTO.AMC.txt

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77 taggaggcat acaactccag gttgatctgg cggttgatgg cagcctccga gtcctggtgg
78 tagttctggc gcacttgcga gggagacgcg gtggtcatga tggcggctgg acgaggcgcg
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80 gacggggtc ggagggtcg agcaccgggt tccgttcaag cactgttgaa gcaggaaacc
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81 gcggcgactc tgggcgagaa cgtctggcgt agggaccagc gggccgcact ttatagcggg
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82 atcctgcgtc aggcgcgctc cggccaatca gcgcggtggg ccgcccagcc ccgcctcttc
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83 ctgtaggcgt gttgcccaag ccagcagtgc gtgggcgggg aggagcctgt gtgattgtga
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                                                            Ser Cys
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100 tat ttt gac cgg gat gat gtg gcc ctg aag aac ttt gcc aaa tac ttt
101 Tyr Phe Asp Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe
102
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                                 10
104 ctc cat caa tct cat gaa gag agg gaa cat gct gag aaa ctg atg aag
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105 Leu His Gln Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys
108 ctg cag aac cag cga ggt gga cga atc ttc ctg cag gat atc aag
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Input Set : A:\PTO.AMC.txt

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Lys Pro Asp Arg Asp Asp Trp 155 157 gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt 158 Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 159 10 15 20 161 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat 162 Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 163 25 30 35 165 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc 169 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt 170 180 181 182 183 184 185 185 186 187 186 181 182 182 183 185 185 186 187 188 188 189 188 180 180 185 181 185 185 186 187 188 188 188 188 188 188	Lys Pro Asp Arg Asp Asp Trp 155 157 gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt 158 Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 159 10 15 20 161 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat 162 Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 163 25 30 35 165 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc 169 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt 169 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt 170 180 181 182 183 184 185 186 187 186 181 182 183 186 187 188 188 188 188 188 188	W>			- 4
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167 40 169 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt 170 Leu Cys 173 gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa 185 174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 185 175 45 50 55 60 187 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 186 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 189 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg	167 40 169 acagggettg ggagagetga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt 170 Leu Cys 173 gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa 185 174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 185 175 45 50 55 60 186 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 187 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg				
Leu Cys 173 gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa 305 174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg	Leu Cys 173 gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa 305 174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg			· · · ·	
173 gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa 174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg	173 gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa 174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 175 45 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 185 80 186 85 90 187 453		169	acagggettg ggagagetga ccagtaacce tgtcccatgt tetettteet ag tta tgt	257
174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 353 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	174 Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 353 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453		170	Leu Cys	
175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 353 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	175 45 50 55 60 177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 353 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453		173	gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa	305
177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	177 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa 178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453		174	Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys	
178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	178 Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453				
179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	179 65 70 75 181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453			344 003 330 340 040 3-3 400 4403- 443 453 334 344 444 3	353
181 tot ggc atg gca gaa tat oto ttt gac aag cac acc otg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gotgacgtoo coaaggocat gtgactttac tggotcactg 453	181 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt 401 182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453				
182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	182 Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453				
183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	183 80 85 90 185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453			220 330 303 300 200 200 200 300 300 300	101
185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453	185 gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg 453				
The gas age and gregore ready to the Jeguera and a special age.	The gar gag age and gregore remaggered greaters aggreened				152
	186 ASP GIU Ser *			gar gag age can geogrape conneggerate geometric eggerates	133
100 Wah Gin Ser .			TRP	Asp Giu Sei *	

Input Set : A:\PTO.AMC.txt

187 95	
189 aggcagtgca tgcatgtcag gctgccttta tcttttctat aagttgcacc aaaacat	tctg 513
190 cttaaaagtt ctttaatttg taccatttct tcaaataaag aattttggta cccagct	
191 gttgtgattg aggatgagcg caccagcttc ccttgcgtcg gctatataac cacactg	
192 cgcctgaaag aatatttatt aaactcgtag ttggggaaag atagtgaaag acaggtg	
193 tcagacagga ctaagcagtc ctggttctga gttacctgcc agactgccat gggaaca	
194 tettgagtgt c	764
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197 <211> LENGTH: 42	•
198 <212> TYPE: PRT	
199 <213> ORGANISM: Rattus norvegicus	
201 <400> SEQUENCE: 8	
202 Lys Pro Asp Arg Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Arg Cy	ys
203 1 5 10 15	
204 Ala Leu His Leu Glu Lys Ser Val Asn Gln Ser Leu Leu Glu Leu H	is
205 20 25 30	
206 Lys Leu Ala Thr Asp Lys Asn Asp Pro His	
207 35 40	
209 <210> SEQ ID NO: 9	
210 <211> LENGTH: 53	
211 <212> TYPE: PRT	
212 <213> ORGANISM: Rattus norvegicus	
214 <400> SEQUENCE: 9	
215 Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Se	er
216 1 5 10 15	
217 Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly A	la
218 20 25 30	
219 Pro Glu Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu G	ly
220 35 40 45	-
221 His Gly Asp Glu Ser	
222 50	
224 <210> SEQ ID NO: 10	
225 <211> LENGTH: 764	
226 <212> TYPE: DNA	
227 <213> ORGANISM: Rattus norvegicus	
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231 gtcctgtctg aacacacctg tctttcacta tctttcccca actacgagtt taataaa	atat 120
232 tettteagge gttgeagtgt ggttatatag cegacgeaag ggaagetggt gegetea	
233 tcaatcacaa caagagctgg gtaccaaaat tctttatttg aagaaatggt acaaatt	taaa 240
234 gaacttttaa gcagatgttt tggtgcaact tatagaaaag ataaaggcag cctgaca	
235 atgcactgcc tcagtgagcc agtaaagtca catggccttg gggacgtcag cttagct	
236 atcaccgtgt cccagggtgt gcttgtcaaa gagatattct gccatgccag attcagg	
237 teceatettg egtaagttgg teaegtggte acceagttet ttaatggatt teaectg	
238 attcaggtaa tgcgtctcaa tgaagtcaca taactaggaa agagaacatg ggacag	
239 actggtcage teteccaage cetgtggcaa ateateteca eteacecegt gtttete	
240 ctcacgtggg gatcattctt gtcagtagcc agtttgtgaa gttccagtag tgactga	attc 660
241 acactettt ccaagtgcag tgcacacete attgcattca gcccgctete ccagte	
242 cggtcaggtt tctgaatcaa agaaacatgt caattcatct gcag	764

Input Set : A:\PTO.AMC.txt

244 <210> SEO ID NO: 11

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245 <211> LENGTH: 2045
    246 <212> TYPE: DNA
    247 <213> ORGANISM: Artificial Sequence
    249 <220> FEATURE:
    250 <223> OTHER INFORMATION: Vector sequence
W--> 252 <221> NAME/KEY: CDS
    253 <222> LOCATION: (1132)...(1279)
W--> 255 <221> CDS
    256 <222> LOCATION: (1495)...(1622)
W--> 258 <221> CDS
    259 <222> LOCATION: (1715)...(1873)
W--> 261 <221> misc feature
    262 <222> LOCATION: (1)...(2045)
    263 <223> OTHER INFORMATION: n = A, T, C or G
W--> 265 <400> 11
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    267 ctcccttggg ccacttggtg agctggcgga gggtgggttg gggcgtggcc tgctgcgggc
                                                                           120
                                                                           180
    268 ttccccgcct tccagcgccc ttctggaaaa tggagtttgt ccggggttct ttccaaaggc
    269 aggcagccct gccgtggcaa gtctgagcac ctagcgcttt gtggctcctg catagaccag
                                                                           240
                                                                           300
    270 gcacqtcata acacccgtgt tttgaagcct tagggctgta caactgtcag cctctccaat
    271 caaccetgca gttaggtgca ttttcctgca ctctcgtccc ctccggtcac atggcctgca
                                                                           360
    272 ggcttctctg tttgggtgta catccagctc cagttcctct gactatggcg ggtctgcttg
    273 gtcatggtgt ggaatggcag ccctggggct tggtacaaag aggcttatct cttgtgaact
                                                                           480
                                                                           540
    274 tactctaacc acttctgaag cagcggcctc tacatctctg cttatcacag agcctcactt
    275 gcattgaaac ttatcgctag gaatctcccc ttctgtaatc accctgacct tgccaaggca
                                                                           600
    276 tctagagtac tgtacgtttt taatttttat tttgcaccag ttgttgctta ctaacagaag
                                                                           660
    277 tagtaggtaa catacttgtt ggaaaaagcc cacggttggg aaaaaaccat tatcgtggaa
                                                                           720
                                                                           780
    278 tacaaataca ctgagtgeet aaaactgaaa atcaaagett eteecaatgt atttgtgeta
    279 aaatacaatg ccctcagttc ttaaccaggt aatcagcagt tggctgtcta gctgaaaacc
                                                                           840
    280 ttgagacctt gtgttaacca ttttttttat ttaacatgat tgttgaagga gagaattgac
                                                                           900
                                                                           960
    281 ctcccaatgt agggcacttt agcaccccc ctctcagaca aatagatatg gccttggctt
    282 aaagtttttt ctctgcacta atgtggagcc atagaaccct tgataaagcc aagtcccaag
                                                                          1020
    283 tttgttttcc catccttact ttaaaggcca agtagggtga caaacagcct ttaccaccat
                                                                          1080
    284 tgcatctgcc ttgctgtggg gatcaataac aaataccctt tccactttca g tct tgt
                                                                          1137
                                                               Ser Cys
    285
    286
                                                                          1185
    288 tat ttt gac egg gat gat gtg gee etg aag aac ttt gee aaa tae ttt
    289 Tyr Phe Asp Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe
    292 ctc cat caa tct cat gaa gag agg gaa cat gct gag aaa ctg atg aag
                                                                          1233
    293 Leu His Gln Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys
    294
             20
                                25
                                                   30
                                                                          1279
    296 ctg cag aac cag cga ggt gga cga atc ttc ctg cag gat atc aag g
    297 Leu Gln Asn Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys
    298
                            40
                                                                          1339
W--> 300 taagtagact atgggactgc gttaaatgag cagtnnnnnn nnnnnnnnn nnnnnnnnnn
                                                                          1399
1459
```

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02092006\J532197.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:11; N Pos. 1314,1315,1316,1317,1318,1319,1320,1321,1322,1323,1324,1325
Seq#:11; N Pos. 1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337
Seq#:11; N Pos. 1338,1339,1340,1341,1342,1343,1344,1345,1346,1347,1348,1349
Seq#:11; N Pos. 1350,1351,1352,1353,1354,1355,1356,1357,1358,1359,1360,1361
Seq#:11; N Pos. 1362,1363,1364,1365,1366,1367,1368,1369,1370,1371,1372,1373
Seq#:11; N Pos. 1374,1375,1376,1377,1378,1379,1380,1381,1382,1383,1384,1385
Seq#:11; N Pos. 1386,1387,1388,1389,1390,1391,1392,1393,1394,1395,1396,1397
Seq#:11; N Pos. 1398,1399,1400,1401,1402,1403,1404,1405,1406,1407,1408,1409
Seq#:11; N Pos. 1410,1411,1412,1413,1414,1415,1416,1417,1418,1419,1420,1421
Seq#:11; N Pos. 1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433
Seq#:11; N Pos. 1434,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445
Seq#:11; N Pos. 1446,1447,1448,1449,1450,1451,1452,1453,1454,1455,1456,1457
Seq#:11; N Pos. 1458,1459,1460,1461,1462,1463
Seq#:34; N Pos. 4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24
Seq#:36; N Pos. 1,2,3,4,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29
Seg#:36; N Pos. 30,31,32,33
Seq#:38; N Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/532,197

DATE: 02/09/2006
TIME: 18:29:58

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02092006\J532197.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:152 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7 L:252 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11 L:258 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11 L:261 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11 L:265 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11 L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1279 L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1339 L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1399 L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1459 L:304 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11 L:695 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34 L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0 L:721 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:725 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0 L:747 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:751 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:38 L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0

Raw Sequence Listing before editing (for reference only)



PCT

RAW SEQUENCE LISTING DATE: 02/09/2006
PATENT APPLICATION: US/10/532,197 TIME: 18:20:36

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02092006\J532197.raw

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4 <110> APPLICANT: Biogen Idec MA Inc.
             Prentice, Holly
     7 <120> TITLE OF INVENTION: HIGH EXPRESSION LOCUS VECTOR BASED ON
              FERRITIN HEAVY CHAIN GENE LOCUS
    11 <130> FILE REFERENCE: 2159.058PC01/EKS/LMB
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/532,197
C--> 13 <141> CURRENT FILING DATE: 2005-04-21
     13 <150> PRIOR APPLICATION NUMBER: PCT/US2003/033433
     14 <151> PRIOR FILING DATE: 2003-10-22
     16 <150> PRIOR APPLICATION NUMBER: US 60/421,252
     17 <151> PRIOR FILING DATE: 2002-10-24
    19 <160> NUMBER OF SEQ ID NOS: 41
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    21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
                                                              Corrected Diskette Needed
    23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 563
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Rattus norvegicus
     28 <220> FEATURE:
     29 <221> NAME/KEY: CDS
    30 <222> LOCATION: (346)...(459)
    32 <400> SEQUENCE: 1
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     34 tggcttgggc aacacgccta caggaagagg cggggctggg cggcccaccg cgctgattgg
                                                                              120
                                                                              180
    35 ccggagegeg cctgacgcag gatcccgcta taaagtgcgg cccgctggtc cctacgccag
                                                                              240
     36 acgttctcgc ccagagtcgc cgcggtttcc tgcttcaaca gtgcttgaac ggaacccggt
                                                                              300
     37 getegaceee teegaceeee gteeggeege tttgageetg ageeetttge aacttegteg
                                                                              357
    38 ctccgccgct ccagcgtcgc ctccgcgcct cgtccagccg ccatc atg acc acc gcg
    39
                                                           Met Thr Thr Ala
     40
                                                                              405
     42 tot ecc tog caa gtg ege cag aac tac cac cag gac tog gag got gee
     43 Ser Pro Ser Gln Val Arg Gln Asn Tyr His Gln Asp Ser Glu Ala Ala
     44 5
                             10
     46 atc aac cgc cag atc aac ctg gag ttg tat gcc tcc tac gtc tat ctg
                                                                              453
     47 Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser Tyr Val Tyr Leu
                                             30
                                                                  35
     48
                         25
                                                                              509
     50 tcc atg gtgagtgcgg cctggccttt gcgggggcgg aaagagggtg cggcctggcc
     51 Ser Met
                                                                              563
     54 tcccttgggc cacttggtga gctggcggag ggtgggttgg ggcgtggctg cggg
     56 <210> SEQ ID NO: 2
     57 <211> LENGTH: 38
     58 <212> TYPE: PRT
     59 <213> ORGANISM: Rattus norvegicus
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61 <400> SEQUENCE: 2

Input Set : A:\PTO.AMC.txt

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62 Met Thr Thr Ala Ser Pro Ser Gln Val Arg Gln Asn Tyr His Gln Asp
64 Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser
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77 taggaggcat acaactccag gttgatctgg cggttgatgg cagcctccga gtcctggtgg
78 taqttctqqc qcacttqcqa qqqaqacqcq qtggtcatga tggcggctgg acgaggcgcg
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79 gaggcgacgc tggagcggcg gagcgacgaa gttgcaaagg gctcaggctc aaagcggccg
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80 gacggggtc ggagggtcg agcaccgggt tccgttcaag cactgttgaa gcaggaaacc
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81 gcggcgactc tgggcgagaa cgtctggcgt agggaccagc gggccgcact ttatagcggg
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82 atcctgcgtc aggcgcgctc cggccaatca gcgcggtggg ccgcccagcc ccgcctcttc
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83 ctgtaggcgt gttgcccaag ccagcagtgc gtgggcgggg aggagcctgt gtgattgtga
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87 <211> LENGTH: 232
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89 <213> ORGANISM: Rattus norvegicus
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93 <222> LOCATION: (51)...(197)
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                                                            Ser Cys
98
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100 tat ttt gac cgg gat gat gtg gcc ctg aag aac ttt gcc aaa tac ttt
101 Tyr Phe Asp Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe
                                 10
104 ctc cat caa tct cat gaa gag agg gaa cat gct gag aaa ctg atg aag
                                                                          152
105 Leu His Gln Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys
108 ctg cag aac cag cga ggt gga cga atc ttc ctg cag gat atc aag
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109 Leu Gln Asn Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys
110 35
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121 1
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Input Set : A:\PTO.AMC.txt

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	155		
		1 5	
			L02
	157	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt	L02
	157		L02
	157 158 159	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20	L02 L50
	157 158 159 161	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20	
	157 158 159 161 162 163	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35	150
	157 158 159 161 162 163 165	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc	
	157 158 159 161 162 163 165 166	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His	150
	157 158 159 161 162 163 165 166	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40	150
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	157 158 159 161 162 163 165 166 167 169 170	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys	150 199 257
	157 158 159 161 162 163 165 166 167 169 170	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa	150
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	157 158 159 161 162 163 165 166 167 169 170 173 174 175	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60	150 199 257
	157 158 159 161 162 163 165 166 167 170 173 174 175 177	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa	150 199 257
	157 158 159 161 162 163 165 166 167 170 173 174 175 177	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60	150 199 257
	157 158 159 161 162 163 165 166 167 170 173 174 175 177 178 179 181	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacacggg gtgagtggag atgattgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 65 70 75 tct ggc atg gca gag gad cac ggt	150 199 257
	157 158 159 161 162 163 165 166 167 170 173 174 175 177 178 179 181	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 65 70 75 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly	150 199 257 305
	157 158 159 161 162 163 165 166 167 170 173 174 175 177 178 179 181 182	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 65 70 75 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 80 85 90	150 199 257 305 353
	157 158 159 161 162 163 165 166 167 173 174 175 177 178 181 182 183 185	gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag agt Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser 10 15 20 gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn 25 30 35 gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc Asp Pro His 40 acagggcttg ggagagctga ccagtaaccc tgtcccatgt tctctttcct ag tta tgt Leu Cys gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys 45 50 55 60 gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu 65 70 75 tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly 80 85 90	150 199 257 305

Input Set : A:\PTO.AMC.txt

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	gttgtgattg aggatgagcg caccagette cettgegteg getatataac cacactgcaa	633
	cgcctgaaag aatatttatt aaactcgtag ttggggaaag atagtgaaag acaggtgtgt	693
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	acactetttt ccaagtgeag tgeacacete attgeattea geeegetete ecagteatea	720
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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02092006\J532197.raw

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     263 <223 > OTHER INFORMATION: n = A, T, C or G
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                                                                             300
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    285
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     288 tat ttt gac egg gat gat gtg gee etg aag aac ttt gee aaa tac ttt
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     289 Tyr Phe Asp Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe
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    292 ctc cat caa tct cat gaa gag agg gaa cat gct gag aaa ctg atg aag
    293 Leu His Gln Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys
    294
             20
                                 25
                                                     30
     296 ctg cag aac cag cga ggt gga cga atc ttc ctg cag gat atc aag g
                                                                            1279
     297 Leu Gln Asn Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys
    298
                             40
W--> 300 taagtagact atgggactgc gttaaatgag cagtnnnnnn nnnnnnnnn nnnnnnnnn
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                                                                            1399
1459
```

from Sequere 11

10/532,197

Lys Pro Asp Arg Asp Asp

tgg gag agc ggg ctg aat gca atg agg tgt gca ctg cac ttg gaa aag Trp Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys £0-60 · ·

1562

mesaligned humbering began here and continued throughout the sequence £5. (05

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02092006\J532197.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:11; N Pos. 1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337
Seq#:11; N Pos. 1338,1339,1340,1341,1342,1343,1344,1345,1346,1347,1348,1349
Seq#:11; N Pos. 1350,1351,1352,1353,1354,1355,1356,1357,1358,1359,1360,1361
Seq#:11; N Pos. 1362,1363,1364,1365,1366,1367,1368,1369,1370,1371,1372,1373
Seq#:11; N Pos. 1374,1375,1376,1377,1378,1379,1380,1381,1382,1383,1384,1385
Seq#:11; N Pos. 1386,1387,1388,1389,1390,1391,1392,1393,1394,1395,1396,1397
Seq#:11; N Pos. 1398,1399,1400,1401,1402,1403,1404,1405,1406,1407,1408,1409
Seq#:11; N Pos. 1410,1411,1412,1413,1414,1415,1416,1417,1418,1419,1420,1421
Seq#:11; N Pos. 1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433
Seq#:11; N Pos. 1434,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445
Seq#:11; N Pos. 1446,1447,1448,1449,1450,1451,1452,1453,1454,1455,1456,1457
Seq#:11; N Pos. 1458,1459,1460,1461,1462,1463
Seq#:34; N Pos. 4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24
Seq#:36; N Pos. 1,2,3,4,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29
Seq#:36; N Pos. 30,31,32,33
Seq#:38; N Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
```

VERIFICATION SUMMARY DATE: 02/09/2006 PATENT APPLICATION: US/10/532,197 TIME: 18:20:37

Input Set : A:\PTO.AMC.txt

```
L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:152 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:252 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:258 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:261 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:265 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:300~M:341~W:~(46)~"n" or "Xaa" used, for SEQ ID#:11 after pos.:1279
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1339
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1399
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1459
L:304 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:317 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:333 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:695 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:721 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:725 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:747 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:751 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:38
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
```